Freeform Search

Database: US Pre-Grant Publication Full-Text Database; US Patents Full-Text Database; US OCR Full-Text Database; EPO Abstracts Database; JPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Term: L7 and (detect$3 or determin$3)

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Search Clear Interrupt

Search History

DATE: Thursday, March 01, 2007 Purge Queries Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ			
L8	L7 and (detect$3 or determin$3)	37	L8
L7	L6 and ((mu near5 system) or (mu near5 transposase$1))	38	L7
L6	transposit$4 near5 (muta$4 or mismatch$2 or delet$3 or insert$3)	1166	L6
L5	detect$3 near5 (muta$5 or mismatch$2 or delet$3 or insert$3) near5 transpons$2	0	L5
L4	l3 and ((mu near5 transposase$1)or (mu near5 nucleic acid))	12	L4
L3	L2 and ((detect$3 or determin$3) near5 (mismatch$3 or insert$3 or delet$3 or muta$4))	145	L3
L2	L1 and (transpos$3 near5 site$1 near5 (mismatch$2 or delet$3 or insert$3))	264	L2
L1	transposit$3 and detect$3 and (mismatch$2 or insert$3 or delet$3)	6413	L1

END OF SEARCH HISTORY

STN search

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 s l8 and transposase#
L9            4 L8 AND TRANSPOSASE#

=> d l9 1-4 bib ab kwic

L9   ANSWER 1 OF 4     MEDLINE on STN
AN   2002432274     MEDLINE
DN   PubMed ID: 12177413
TI   Mismatch-targeted transposition of Mu: a new strategy
     to map genetic polymorphism.
AU   Yanagihara Katsuhiko; Mizuuchi Kiyoshi
CS   Laboratory of Molecular Biology, National Institute of Diabetes, Digestive
     and Kidney Diseases, National Institutes of Health, Bethesda, MD 20892,
     USA.
SO   Proceedings of the National Academy of Sciences of the United States of
     America, (2002 Aug 20) Vol. 99, No. 17, pp. 11317-21. Electronic
     Publication: 2002-08-12.
     Journal code: 7505876. ISSN: 0027-8424.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
     (RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LA   English
FS   Priority Journals
EM   200209
ED   Entered STN: 22 Aug 2002
     Last Updated on STN: 5 Jan 2003
     Entered Medline: 27 Sep 2002
AB   Phage Mu DNA transposes to duplex target DNA sites with limited sequence
     specificity. Here we demonstrate that Mu transposition exhibits a strong
     target site preference for all single-nucleotide mismatches. This finding
     has implications for the mechanism of transposition and provides a
     powerful tool for genomic research. A single mismatch could be
     detected as a preferred target of Mu
     transposition in the presence of 300,000-fold excess of
     nonmismatched sites. We demonstrate the detection of both heterozygous
     and homozygous mutations in the cystic fibrosis transmembrane conductance
     regulator gene and single nucleotide polymorphism in HLA region by Mu
     transposition mismatch analysis procedure.
TI   Mismatch-targeted transposition of Mu: a new strategy
     to map genetic polymorphism.
AB   . . . mismatches. This finding has implications for the mechanism of
     transposition and provides a powerful tool for genomic research. A single
     mismatch could be detected as a preferred target
     of Mu transposition in the presence of 300,000-fold excess of
     nonmismatched sites. We demonstrate the detection of both heterozygous
     and homozygous mutations in the cystic fibrosis transmembrane conductance
     regulator gene and single nucleotide polymorphism in HLA region by Mu
     transposition mismatch analysis procedure.
CT    . . . GE, genetics
      Cystic Fibrosis Transmembrane Conductance Regulator: GE, genetics
      DNA, Viral: GE, genetics
      Humans
      Molecular Sequence Data
      Oligodeoxyribonucleotides
     *Polymorphism, Genetic
       *Transposases: GE, genetics
CN   0 (CFTR protein, human); 0 (DNA, Viral); 0 (Oligodeoxyribonucleotides); EC
     2.7.- (mu transposase); EC 2.7.7.- (Transposases)

L9   ANSWER 2 OF 4     MEDLINE on STN
AN   93211299     MEDLINE
DN   PubMed ID: 8096321
TI   Identification and characterization of IS1138, a transposable element from
```

Mycoplasma pulmonis that belongs to the IS3 family.
AU Bhugra B; Dybvig K
CS Department of Microbiology, University of Alabama, Birmingham 35294.
NC AI31144 (NIAID)
P30 AI27767 (NIAID)
SO Molecular microbiology, (1993 Feb) Vol. 7, No. 4, pp. 577-84.
Journal code: 8712028. ISSN: 0950-382X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LA English
FS Priority Journals
OS GENBANK-Z16416
EM 199304
ED Entered STN: 14 May 1993
Last Updated on STN: 29 Jan 1999
Entered Medline: 27 Apr 1993
AB Insertion sequence (IS) elements are mobile genetic elements found in prokaryotes. We have identified a repetitive element from Mycoplasma pulmonis, a murine pathogen, that is similar to eubacterial IS elements. By subcloning a single strain of M. pulmonis, we isolated a variant clone in which the IS element had undergone an apparent transposition event. The nucleotide sequences of the element, designated IS1138, and the target site into which it inserted were determined. IS1138 consists of 1288 bp with 18 bp perfect terminal inverted repeats. Sequence analysis of the target site before and after insertion of IS1138 identified a 3 bp duplication of target DNA flanking the element. The predicted amino acids encoded by the major open reading frame of IS1138 share significant similarity with the transposases of the IS3 family. Southern hybridization analysis indicates that repetitive sequences similar to IS1138 are present in most, if not all, strains of M. pulmonis, but IS1138-like sequences were not detected in other mycoplasmal species.
AB . . . murine pathogen, that is similar to eubacterial IS elements. By subcloning a single strain of M. pulmonis, we isolated a variant clone in which the IS element had undergone an apparent transposition event. The nucleotide sequences of the element, designated IS1138, and the target site into which it inserted were determined. IS1138 consists of 1288 bp with 18 bp perfect terminal inverted repeats. Sequence analysis of the target site before and. . . the element. The predicted amino acids encoded by the major open reading frame of IS1138 share significant similarity with the transposases of the IS3 family. Southern hybridization analysis indicates that repetitive sequences similar to IS1138 are present in most, if not. . .
CT . . . genetics
Polymerase Chain Reaction
Polymorphism, Restriction Fragment Length
Repetitive Sequences, Nucleic Acid: GE, genetics
Sequence Homology, Amino Acid
Species Specificity
Transposases
CN 0 (DNA Transposable Elements); EC 2.7.7.- (Nucleotidyltransferases); EC 2.7.7.- (Transposases)

L9 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2007 ACS on STN
AN 2004:803873 CAPLUS
DN 141:290033
TI Methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis
IN Yanagihara, Katsuhiko; Mizuuchi, Kiyoshi
PA United States Dept. of Health and Human Services, USA

SO U.S. Pat. Appl. Publ., 24 pp.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 2004191821	A1	20040930	US 2004-809688	20040326
PRAI US 2003-457934P	P	20030328		

AB Phage Mu DNA transposes to duplex target DNA sites with limited sequence specificity. The present invention provides methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microbes using mismatch-targeted Mu transposition for use in diagnosis.
Mu transposition exhibits a strong target site preference for all single-nucleotide mismatches. This finding has implications for the mechanism of transposition and provides a powerful tool for genomic research. A single mismatch could be detected as a preferred target of Mu transposition in the presence of 300,000-fold excess of non-mismatched sites. Both heterozygous and homozygous mutations in the cystic fibrosis transmembrane conductance regulator gene and single nucleotide polymorphism in HLA region were detected by Mu transposition mismatch anal. procedure.

TI Methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis

AB Phage Mu DNA transposes to duplex target DNA sites with limited sequence specificity. The present invention provides methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microbes using mismatch-targeted Mu transposition for use in diagnosis.
Mu transposition exhibits a strong target site preference for all single-nucleotide mismatches. This finding has implications for the mechanism of transposition and provides a powerful tool for genomic research. A single mismatch could be detected as a preferred target of Mu transposition in the presence of 300,000-fold excess of non-mismatched sites. Both heterozygous and homozygous mutations in the cystic fibrosis transmembrane conductance regulator gene and single nucleotide polymorphism in HLA region were detected by Mu transposition mismatch anal. procedure.

ST mismatch targeted transposition phage Mu detection polymorphism mutation; gene HLA CFTR phage Mu transposition cancer diagnosis pathogen

IT Gene, animal
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(APC, mutation in; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT Gene, animal
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(BRCA1, mutation in; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT Gene, animal
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(CFTR, mutation in; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT Gene, animal

RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(HLA, mutation in; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT Gene, animal
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(HMLH1, mutation in; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT Gene, animal
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(HMSH1, mutation in; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT Gene, animal
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(RB1, mutation in; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT Gene, animal
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(TP53; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT Gel electrophoresis
(acrylamide or agarose; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT Diagnosis
(cancer; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT Gel electrophoresis
(capillary; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT Pathogen
(detection of; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT Capillary electrophoresis
(gel; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT Enterobacteria phage Mu
High throughput screening
Human
Mutation
Neoplasm
PCR (polymerase chain reaction)
Susceptibility (genetic)
Tumor markers
(methods for detecting genetic polymorphisms associated with cancer and

for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT Diagnosis
(mol.; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch -targeted Mu transposition for use in diagnosis)

IT Genetic polymorphism
(single nucleotide; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT Enzymes, biological studies
RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(transposases, My; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT Recombination, genetic
(transposition; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT 79-06-1, Acrylamide, biological studies 9012-36-6, Agarose
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(gel electrophoresis; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

IT 763155-35-7 763155-36-8 763155-37-9 763155-38-0 763155-39-1
763155-40-4 763155-41-5 763155-42-6
RL: PRP (Properties)
(unclaimed nucleotide sequence; methods for detecting genetic polymorphisms associated with cancer and for typing pathogenic microorganisms using mismatch-targeted Mu transposition for use in diagnosis)

L9 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2007 ACS on STN
AN 2003:482975 CAPLUS
DN 139:144848
TI Target DNA Bending is an Important Specificity Determinant in Target Site Selection in Tn10 Transposition
AU Pribil, Patrick A.; Haniford, David B.
CS Department of Biochemistry, University of Western Ontario, London, ON, Can.
SO Journal of Molecular Biology (2003), 330(2), 247-259
CODEN: JMOBAK; ISSN: 0022-2836
PB Elsevier Science Ltd.
DT Journal
LA English
AB The bacterial transposon Tn10 inserts preferentially into specific DNA sequences. DNA footprinting and interference studies have revealed that the Tn10-encoded transposase protein contacts a large stretch of target DNA (.apprx.24 bp) and that the target DNA structure is deformed upon incorporation into the transpososome. Target DNA deformation might contribute significantly to target site selection

and thus it is of interest to further define the nature of this deformation. Circular permutation anal. was used to demonstrate that the target DNA is bent upon its incorporation into the transpososome. Two lines of evidence are presented that target DNA bending is an important event in target site selection. First, we demonstrate a correlation between increased target site usage and an increased level of target DNA bending. Second, transposase mutants with relaxed target specificity are shown to cause increased target DNA bending relative to wild-type transposase. This latter observation provides new insight into how relaxed specificity may be achieved. We also show that Ca2+ facilitates target capture by stabilizing transposase interactions with sequences immediately flanking the insertion site. Ca2+ could, in theory, exert this effect by stabilizing bends in the target DNA.

RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

AB The bacterial transposon Tn10 inserts preferentially into specific DNA sequences. DNA footprinting and interference studies have revealed that the Tn10-encoded transposase protein contacts a large stretch of target DNA (.apprx.24 bp) and that the target DNA structure is deformed upon incorporation into the transpososome. Target DNA deformation might contribute significantly to target site selection and thus it is of interest to further define the nature of this deformation. Circular permutation anal. was used to demonstrate that the target DNA is bent upon its incorporation into the transpososome. Two lines of evidence are presented that target DNA bending is an important event in target site selection. First, we demonstrate a correlation between increased target site usage and an increased level of target DNA bending. Second, transposase mutants with relaxed target specificity are shown to cause increased target DNA bending relative to wild-type transposase. This latter observation provides new insight into how relaxed specificity may be achieved. We also show that Ca2+ facilitates target capture by stabilizing transposase interactions with sequences immediately flanking the insertion site. Ca2+ could, in theory, exert this effect by stabilizing bends in the target DNA.

ST Tn10 transposon transposase DNA bending calcium insertion site

IT Genetic element
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(insertion site of transposon; target DNA Bending is an Important Specificity Determinant in Target Site Selection in Tn10 Transposition)

IT Enzymes, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(transposases; target DNA Bending is an Important Specificity Determinant in Target Site Selection in Tn10 Transposition)

IT 7440-70-2, Calcium, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(affecting recognition of transposition site by transposase; target DNA Bending is an Important Specificity Determinant in Target Site Selection in Tn10 Transposition)

=>

(FILE 'HOME' ENTERED AT 15:38:27 ON 01 MAR 2007)

FILE 'MEDLINE, CAPLUS, EMBASE, BIOSIS' ENTERED AT 15:38:58 ON 01 MAR 2007

L1 488 S TARGET#(10A)(MISMATCH## OR VARIANT## OR DELET### OR INSERT###
L2 2549 S TRANSPOSIT####(10A)(MISMATCH## OR VARIANT## OR DELET### OR IN
L3 1 S 1L AND L2
L4 1 S L1 AND (MU(5A)SYSTEM OR MU(10A)TRANSPOSASE#)
L5 27 S L1 AND (TRANSPOS#####(10A)(DELET### OR INSERT### OR MUTA#####
L6 5 S L5 AND MU
L7 2 DUP REM L6 (3 DUPLICATES REMOVED)
L8 11 DUP REM L5 (16 DUPLICATES REMOVED)
L9 4 S L8 AND TRANSPOSASE#